



- 1 -

SEQUENCE LISTING

<110> Civelli, Olivier
Nothacker, Hans-Peter
Wang, Zhiwei
Reinscheid, Rainer

<120> ADP-Glucose Receptor

<130> P-UC 4530

<140> US 09/780,576

<141> 2001-02-09

<150> US 60/234,025

<151> 2000-09-20

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<212> DNA

<213> Homo sapiens

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Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu Cys Thr
5 10 15

aga gac tac aaa atc acc cag gtc ctc ttc cca ctg ctc tac act gtc 153
Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr Thr Val
20 25 30

ctg ttt ttt gtt gga ctt atc aca aat ggc ctg gcg atg agg att ttc 201
Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg Ile Phe
35 40 45 50

ttt caa atc cgg agt aaa tca aac ttt att att ttt ctt aag aac aca 249
Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys Asn Thr
55 60 65

gtc att tct gat ctt ctc atg att ctg act ttt cca ttc aaa att ctt	297
Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys Ile Leu	
70 75 80	
agt gat gcc aaa ctg gga aca gga cca ctg aga act ttt gtg tgt caa	345
Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val Cys Gln	
85 90 95	
gtt acc tcc gtc ata ttt tat ttc aca atg tat atc agt att tca ttc	393
Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile Ser Phe	
100 105 110	
ctg gga ctg ata act atc gat cgc tac cag aag acc acc agg cca ttt	441
Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg Pro Phe	
115 120 125 130	
aaa aca tcc aac ccc aaa aat ctc ttg ggg gct aag att ctc tct gtt	489
Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu Ser Val	
135 140 145	
gtc atc tgg gca ttc atg ttc tta ctc tct ttg cct aac atg att ctg	537
Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met Ile Leu	
150 155 160	
acc aac agg cag ccg aga gac aag aat gtg aag aaa tgc tct ttc ctt	585
Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser Phe Leu	
165 170 175	
aaa tca gag ttc ggt cta gtc tgg cat gaa ata gta aat tac atc tgt	633
Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr Ile Cys	
180 185 190	
caa gtc att ttc tgg att aat ttc tta att gtt att gta tgt tat aca	681
Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys Tyr Thr	
195 200 205 210	
ctc att aca aaa gaa ctg tac cgg tca tac gta aga acg agg ggt gta	729
Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg Gly Val	
215 220 225	
ggg aaa gtc ccc agg aaa aag gtg aac gtc aaa gtt ttc att atc att	777
Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile Ile Ile	
230 235 240	
gct gta ttc ttt att tgt ttt gtt cct ttc cat ttt gcc cga att cct	825
Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg Ile Pro	
245 250 255	
tac acc ctg agc caa acc cgg gat gtc ttt gac tgc act gct gaa aat	873
Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala Glu Asn	
260 265 270	
act ctg ttc tat gtg aaa gag agc act ctg tgg tta act tcc tta aat	921

Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser Leu Asn
275 280 285 290

gca tgc ctg gat ccg ttc atc tat ttt ttc ctt tgc aag tcc ttc aga 969
Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser Phe Arg
295 300 305

aat tcc ttg ata agt atg ctg aag tgc ccc aat tct gca aca tct ctg 1017
Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr Ser Leu
310 315 320

tcc cag gac aat agg aaa aaa gaa cag gat ggt ggt gac cca aat gaa 1065
Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro Asn Glu
325 330 335

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35 40 45
Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
50 55 60
Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
65 70 75 80
Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
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Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
100 105 110
Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
115 120 125
Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
130 135 140
Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
145 150 155 160
Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
165 170 175
Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
180 185 190
Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
195 200 205

Tyr	Thr	Leu	Ile	Thr	Lys	Glu	Leu	Tyr	Arg	Ser	Tyr	Val	Arg	Thr	Arg
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Gly	Val	Gly	Lys	Val	Pro	Arg	Lys	Lys	Val	Asn	Val	Lys	Val	Phe	Ile
225						230				235					240
Ile	Ile	Ala	Val	Phe	Phe	Ile	Cys	Phe	Val	Pro	Phe	His	Phe	Ala	Arg
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Ile	Pro	Tyr	Thr	Leu	Ser	Gln	Thr	Arg	Asp	Val	Phe	Asp	Cys	Thr	Ala
			260					265					270		
Glu	Asn	Thr	Leu	Phe	Tyr	Val	Lys	Glu	Ser	Thr	Leu	Trp	Leu	Thr	Ser
		275					280					285			
Leu	Asn	Ala	Cys	Leu	Asp	Pro	Phe	Ile	Tyr	Phe	Phe	Leu	Cys	Lys	Ser
	290					295				300					
Phe	Arg	Asn	Ser	Leu	Ile	Ser	Met	Leu	Lys	Cys	Pro	Asn	Ser	Ala	Thr
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Ser	Leu	Ser	Gln	Asp	Asn	Arg	Lys	Lys	Glu	Gln	Asp	Gly	Gly	Asp	Pro
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